



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number 151739

TO: Nita M Minnifield  
Location: Rem-3C01&3C18  
Art Unit: 1645  
Wednesday, April 27, 2005  
  
Case Serial Number: 09/508967

From: Toby Port  
Location: Biotech-Chem Library  
REM1-A59  
Phone: 272-2523  
  
toby.port@uspto.gov

### Search Notes

Dear Examiner Minnifield,

Here are the results of your search.  
Please feel free to contact me if you have any questions.

Toby Port

*Reviewed  
5/5/05  
mm*

151739

From: Chan, Christina  
Sent: Tuesday, April 26, 2005 2:09 PM  
To: Minnifield, Nita; STIC-Biotech/ChemLib  
Subject: RE: rush sequence search

Please rush. Thanks Chris

CRFE

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

-----Original Message-----

From: Minnifield, Nita  
Sent: Tuesday, April 26, 2005 7:10 AM  
To: Chan, Christina  
Subject: rush sequence search

Christina, please approve, 2 month amdt.

STIC

09/508967

Please do a commercial and interference sequence search on  
SEQ ID NO: 1 of the above application.

Please search aa 1-415 of SEQ ID NO: 1 and aa 79-415 of SEQ  
ID NO: 1.

Please provide a paper copy of the results.

Thanks,  
Minnifield  
71976

\*\*\*\*\*  
STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 26, 2005, 18:03:03 ; Search time 31.4393 Seconds

(Without alignments)  
3567.329 Million cell updates/sec

Title: US-09-508-967-1\_COPY\_79\_415

Perfect score: 1884  
Sequence: 1 PCKDKGKGVDRSVYEQA.....GSYEWIDNQRKPKDKKXY 337

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubppa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep:\*

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9: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubppa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubppa/US09C\_NEW\_PUB.pep:\*

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15: /cgn2\_6/ptodata/1/pubppa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/1/pubppa/US10C\_PUBCOMB.pep:\*

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19: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	885	47.0	2710	US-10-153-273-12	Sequence 12, Appl
2	845	44.9	700	US-10-153-273-10	Sequence 10, Appl
3	653	34.7	3542	US-10-087-013-2	Sequence 2, Appl
4	379.5	20.1	362	US-10-153-273-18	Sequence 18, Appl
5	360.5	19.1	411	US-10-153-273-19	Sequence 19, Appl
6	308.5	16.4	1143	US-09-924-154-14	Sequence 14, Appl
7	281	14.9	1435	US-10-153-273-4	Sequence 4, Appl
8	280.5	14.9	749	US-10-153-273-6	Sequence 6, Appl
9	280.5	14.9	1086	US-09-924-154-15	Sequence 15, Appl
10	270	14.3	616	US-10-293-913A-4	Sequence 4, Appl
11	269	14.3	616	US-10-293-913A-2	Sequence 2, Appl
12	269	14.3	1421	US-09-924-154-13	Sequence 13, Appl
13	241	12.8	921	US-10-153-273-8	Sequence 8, Appl

14	235	12.5	972	US-09-924-154-16	Sequence 16, Appl
15	229.5	12.2	311	US-10-087-013-10	Sequence 10, Appl
16	220	11.7	407	US-10-087-013-8	Sequence 8, Appl
17	218	11.6	308	US-10-087-013-11	Sequence 11, Appl
18	216.5	11.5	1501	US-09-924-154-17	Sequence 17, Appl
19	216.5	11.5	1568	US-10-712-533A-12	Sequence 12, Appl
20	213.5	11.3	351	US-10-087-013-9	Sequence 9, Appl
21	207	11.0	1115	US-10-153-273-2	Sequence 2, Appl
22	205	10.9	294	US-10-087-013-7	Sequence 7, Appl
23	197.5	10.5	411	US-10-153-273-20	Sequence 20, Appl
24	159.5	8.5	282	US-10-153-273-15	Sequence 15, Appl
25	158.5	8.4	277	US-10-153-273-16	Sequence 16, Appl
26	128.5	6.8	448	US-10-153-668-370	Sequence 370, Appl
27	126	6.7	291	US-10-153-273-13	Sequence 13, Appl
28	121	6.4	311	US-10-153-273-21	Sequence 21, Appl
29	117.5	6.2	754	US-10-153-668-234	Sequence 234, Appl
30	115.5	6.1	281	US-10-424-599-145507	Sequence 145507, Appl
31	115	6.1	324	US-10-153-273-17	Sequence 17, Appl
32	111	5.9	1257	US-10-408-765A-1486	Sequence 1486, Appl
33	108	5.7	665	US-09-820-843A-107	Sequence 107, Appl
34	107.5	5.7	1064	US-10-220-510-1	Sequence 1, Appl
35	107	5.7	284	US-10-424-599-144189	Sequence 144189, Appl
36	106.5	5.7	1002	US-10-654-416-4	Sequence 4, Appl
37	105	5.6	1154	US-09-963-137-203	Sequence 203, Appl
38	105	5.6	1154	US-09-962-854A-4	Sequence 203, Appl
39	105	5.6	1154	US-09-963-137-203	Sequence 203, Appl
40	104.5	5.5	1429	US-10-424-599-227559	Sequence 227559, Appl
41	104.5	5.5	1429	US-09-953-407-1	Sequence 1, Appl
42	102.5	5.4	905	US-10-437-963-152106	Sequence 152106, Appl
43	102	5.4	578	US-09-925-300-1496	Sequence 1496, Appl
44	102	5.4	706	US-10-104-047-3843	Sequence 3843, Appl
45	102	5.4	1179	US-09-821-883-29	Sequence 29, Appl

#### ALIGNMENTS

RESULT 1  
US-10-153-273-12  
Sequence 12, Application US/10153273  
Publication No. US20020169305A1  
GENERAL INFORMATION:  
APPLICANT: Sim, Kim L.  
Chitnise, Chetan  
Miller, Louis H.  
Peterson, David S.  
Su, Xin-zhuan  
Wellens, Thomas E.  
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobe Martens Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: California  
COUNTRY: US  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/153, 273  
FILING DATE: 21-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/210, 288  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Fuller, Michael  
REGISTRATION NUMBER: 36,516

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OM protein - protein search, using bw model

Run on: April 26, 2005, 17:50:53 ; Search time 9.16007 Seconds

(without alignments)  
2746.348 Million cell updates/sec

Title: US-09-508-967-1\_COPY\_79\_415

Perfect score: 1884  
Sequence: 1 PCKKDKGNVDRESVGEA.....GSYENWIDNQRKQPKQKXY 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	892.5	47.4	2182	2	US-08-487-826B-16
2	885	47.0	2710	2	US-08-568-459A-12
3	885	47.0	2710	2	US-08-487-826B-12
4	885	47.0	2710	3	US-09-210-288-12
5	885	47.0	3060	2	US-08-487-826B-14
6	845	44.9	700	2	US-08-568-459A-10
7	845	44.9	700	2	US-08-487-826B-10
8	845	44.9	700	3	US-09-210-288-10
9	379.5	20.1	362	2	US-08-568-459A-18
10	379.5	20.1	362	2	US-08-487-826B-30
11	379.5	20.1	362	3	US-09-210-288-18
12	360.5	19.1	411	2	US-08-568-459A-19
13	360.5	19.1	411	2	US-08-487-826B-31
14	360.5	19.1	411	3	US-09-210-288-19
15	281	14.9	1435	2	US-08-568-459A-4
16	281	14.9	1435	2	US-08-487-826B-4
17	281	14.9	1435	2	US-09-210-288-4
18	280.5	14.9	749	2	US-08-568-459A-6
19	280.5	14.9	749	3	US-08-487-826B-6
20	280.5	14.9	749	3	US-09-210-288-6
21	241	12.8	921	2	US-08-568-459A-8
22	241	12.8	921	2	US-08-487-826B-8
23	241	12.8	921	3	US-09-210-288-8
24	207	11.0	1115	2	US-08-568-459A-2
25	207	11.0	1115	2	US-08-487-826B-2
26	207	11.0	1115	3	US-09-210-288-2
27	207	11.0	1115	6	5198347-6

28	207	11.0	1115	6	5198347-6	Patent No. 5198347
29	197.5	10.5	411	2	US-08-568-459A-20	Sequence 20, App1
30	197.5	10.5	411	2	US-08-487-826B-32	Sequence 32, App1
31	197.5	10.5	411	3	US-09-210-288-20	Sequence 20, App1
32	159.5	8.5	282	2	US-08-568-459A-16	Sequence 16, App1
33	159.5	8.5	282	2	US-08-487-826B-28	Sequence 28, App1
34	159.5	8.5	282	3	US-09-210-288-16	Sequence 16, App1
35	158.5	8.4	277	2	US-08-568-459A-15	Sequence 15, App1
36	158.5	8.4	277	2	US-08-487-826B-27	Sequence 27, App1
37	158.5	8.4	277	3	US-09-210-288-15	Sequence 15, App1
38	150	8.0	197	6	5198347-2	Patent No. 5198347
39	150	8.0	197	6	5198347-2	Patent No. 5198347
40	150	8.0	778	6	5198347-4	Patent No. 5198347
41	150	8.0	778	6	5198347-4	Patent No. 5198347
42	126	6.7	291	2	US-08-568-459A-13	Sequence 13, App1
43	126	6.7	291	2	US-08-487-826B-25	Sequence 25, App1
44	126	6.7	291	3	US-09-210-288-13	Sequence 13, App1
45	121	6.4	311	2	US-08-568-459A-21	Sequence 21, App1

#### ALIGNMENTS

RESULT 1  
US-08-487-826B-16  
Sequence 16, Application US/08487826B  
Patent No. 5993827  
GENERAL INFORMATION:  
APPLICANT: Sim, Kim L.  
APPLICANT: Chitnis, Chetan  
APPLICANT: Miller, Louis H.  
APPLICANT: Peterson, David S.  
APPLICANT: Su, Xin-zhaun  
APPLICANT: Wellens, Thomas E.  
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX  
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Knobbe Martens Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: California  
COUNTRY: US  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,826B  
FILING DATE: 10-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelson, Ned  
REGISTRATION NUMBER: 29, 655  
REFERENCE/DOCKET NUMBER: NIH121.001CP1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2182 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-487-826B-16  
Query Match 47.4%, Score 892.5, DB 2, Length 2182;

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OM protein - protein search, using sw model

Run on: April 26, 2005, 17:50:52 ; Search time 40.9376 Seconds  
(without alignments)  
4215.459 Million cell updates/sec

Title: US-09-508-967-1\_COPY\_79\_415

Perfect score: 1884  
Sequence: 1 FCKKDGKNDVDRFSVKEQA.....GSYENWIDNOKRQDPKQKCY 337

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_tramb1:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1876	99.6	2228	2	060991 plasmodium
2	1160.5	61.6	2275	2	081BX2 plasmodium
3	1123.5	59.6	2215	2	081BX3 plasmodium
4	1085.5	55.2	2215	2	081BW9 plasmodium
5	1039.5	55.2	2209	2	09U066 plasmodium
6	1020.5	54.2	2264	2	081283 plasmodium
7	1003.5	53.3	2152	2	081FQ5 plasmodium
8	1003.5	53.3	2201	2	081FQ6 plasmodium
9	994	52.8	2267	2	081BX1 plasmodium
10	992.5	52.7	2226	2	081BX6 plasmodium
11	991.5	52.6	2149	2	081FK7 plasmodium
12	988	52.4	2192	2	081BW7 plasmodium
13	945.5	50.2	2277	2	09U065 plasmodium
14	935.5	49.7	2231	2	081I17 plasmodium
15	926	49.2	2231	2	081A54 plasmodium
16	920.5	48.9	2193	2	081FQ2 plasmodium
17	909	48.2	2159	2	081FQ2 plasmodium
18	903.5	48.0	2265	2	081A53 plasmodium
19	903.5	48.0	2270	2	09X2B8 plasmodium
20	894	47.5	2199	2	09G2B6 plasmodium
21	892.5	47.4	2182	2	026034 plasmodium
22	892.5	47.4	2646	2	081220 plasmodium
23	889	47.2	2162	2	081EY1 plasmodium
24	889	47.2	2182	2	081EY1 plasmodium
25	889	47.2	2207	2	081A55 plasmodium
26	885	46.7	3078	2	026031 plasmodium
27	879	46.7	3954	2	06LEV2 plasmodium
28	872	46.3	2287	2	081520 plasmodium
29	868.5	46.1	1711	2	096108 plasmodium
30	868	46.1	1729	2	025734 plasmodium
31	868	46.1	2924	2	025733 plasmodium

ALIGNMENTS

32	863	45.8	2135	2	061077	061077 plasmodium
33	858.5	45.6	2223	2	081D12	081D12 plasmodium
34	854.5	45.4	2241	2	081X37	081X37 plasmodium
35	846.5	44.9	3026	2	026030	026030 plasmodium
36	840.5	44.6	896	2	086MR4	086mr4 plasmodium
37	834.5	44.3	2169	2	097312	097312 plasmodium
38	833.5	44.2	2256	2	0815L5	0815L5 plasmodium
39	824.5	43.8	2270	2	0813R5	0813R5 plasmodium
40	823.5	43.7	2239	2	081BW8	081BW8 plasmodium
41	818	43.4	2268	2	081A55	081A55 plasmodium
42	806.5	42.8	2120	2	081A51	081A51 plasmodium
43	806	42.8	2595	2	081BD8	081BD8 plasmodium
44	798.5	42.4	2163	2	09NFB6	09nfb6 plasmodium
45	794.5	42.2	2209	2	097324	097324 plasmodium

RESULT 1	060991	PRELIMINARY;	PRT;	2228	AA.
ID	060991				
AC	060991;				
DT	01-AUG-1998	(TREMBlrel. 07, Created)			
DT	01-AUG-1998	(TREMBlrel. 07, Last sequence update)			
DT	01-OCT-2003	(TREMBlrel. 25, Last annotation update)			
DE	Erythrocyte membrane protein 1.				
CN	Name=PCR31.2-var1;				
OS	Plasmodium falciparum.				
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.				
NC	NCBI_TaxID=5833;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98080592; PubMed=9419207;				
RA	Chen Q., Barragan A., Fernandez V., Sundstrom A., Schlichterle M.,				
RA	Sahlen A., Carlson J., Datta S., Wahlgren M.,				
RT	Identification of Plasmodium falciparum erythrocyte membrane protein				
RT	1 (PFEMP) as the rosetting ligand of the malaria parasite P.				
RT	falciparum."				
RL	J. Exp. Med. 187:15-23(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Chen Q.J., Wahlgren M.,				
RA	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: AF003473; AAC05730.1; --				
DR	PIR; T14029; T14029.				
DR	GO; GO:0005539; P:glycosaminoglycan binding; IEA.				
DR	GO; GO:0009405; P:patogenesis; IEA.				
DR	InterPro: IPR004258; PFEMP.				
DR	Pfam: PF03011; PFEMP. 2.				
SO	SEQUENCE 2228 AA; 252811 MW; 5D8C8E9BFA22DCB CRC64;				
Query Match					
Best Local Similarity 99.6%; Score 1876; DB 2; Length 2228;					
Matches 336; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY	1	PCKKDGKNDVDRFSVKEQA	YDNRKCKSCNGTCA	PPRRHLICNNP	PNNNSNDSSKAK 60
DB	79	PCKKDGKNDVDRFSVKEQA	YDNRKCKSCNGTCA	PPRRHLICNNP	PNNNSNDSSKAK 138
QY	61	HLILAFCVCAAKYEGESIK	THYPKYDSKPGSDP	PMCTMLARSPADIGI	IGIRDLYLGN 120
DB	139	HLILAFCVCAAKYEGESIK	THYPKYDSKPGSDP	PMCTMLARSPADIGI	IGIRDLYLGN 198
QY	121	KKKKNGKTEREKLEQKLE	IKFKIHNLAKDAKRY	NGDEDPVFLYLRD	MDWTANRE 180
DB	199	KKKKNGKTEREKLEQKLE	IKFKIHNLAKDAKRY	NGDEDPVFLYLRD	MDWTANRE 258
QY	181	TYWGAMTSKELDNSYFRAT	CNDTGQSPSOTHN	CRCDKXGANA	GRPKAGDGVTVIP 240
DB	259	TYWGAMTSKELDNSYFRAT	CNDTGQSPSOTHN	CRCDKXGANA	GRPKAGDGVTVIP 318
QY	241	TYFDVVPOLRWFEEMAD	FCRKKKKKLENTLEK	QCRGKDKSDERYX	CSRNGYDCBOTISR 300

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 26, 2005, 17:50:53 ; Search time 6.55906 Seconds

(without alignments)  
4943.551 Million cell updates/sec

Title: US-09-508-967-1\_COPY\_79\_415

Perfect score: 1884  
Sequence: 1 PCKDGGKNDVDRFSVKEQA.....GSYENWIDNORQDFKQKXY 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79.\*  
2: PIR1.\*  
3: PIR2.\*  
4: PIR3.\*  
5: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1876	99.6	2228	T14029	variant-specific s
2	894	47.5	2197	B71600	variant-specific s
3	892.5	47.4	2182	T28634	variant-specific s
4	885	47.0	3078	T28432	variant-specific s
5	868.5	46.1	1711	T21625	variant-specific s
6	868	46.1	1729	T18396	erythrocyte membra
7	868	46.1	2924	T18378	variant-specific s
8	863	45.8	2135	T14602	variant-specific s
9	846.5	44.9	3026	T28431	variant surface pr
10	789	41.9	2647	T28161	hypothetical prote
11	775	41.1	2212	T28157	erythrocyte membra
12	759	40.3	2664	T28626	variant-specific s
13	707.5	37.6	3006	T28625	variant-specific s
14	680	36.1	2042	T18399	variant-specific s
15	633.5	33.6	2706	T28155	variant-specific s
16	281	14.9	1435	T18373	erythrocyte-bindin
17	207.5	11.0	1045	T18373	erythrocyte-bindin
18	207	11.0	1070	T30848	Duffy receptor - P
19	186.5	9.9	1153	T28652	erythrocyte bindin
20	150	8.0	778	A35970	erythrocyte-bindin
21	117.5	6.2	754	JC5314	CD38/cdc2-like ki
22	114	6.1	1282	JC5314	glycoprotein A - m
23	111	5.9	1257	I58383	retinoblastoma bin
24	111	5.9	1608	T13216	minor capsid prote
25	110.5	5.9	807	T18454	hypothetical prote
26	108	5.7	665	B71609	hypothetical prote
27	108	5.7	4981	T18489	hypothetical prote
28	107	5.7	1199	JC4816	major surface glyco
29	106.5	5.7	590	A25680	nuclear histone-b1

30	106.5	5.7	710	1	I51283	hepatocyte growth
31	106.5	5.7	1002	2	T30546	major surface glyco
32	106.5	5.7	2441	2	D71623	erythrocyte membra
33	105	5.6	508	2	B71620	hypothetical prote
34	104.5	5.5	2116	2	A26655	myosin heavy chain
35	104	5.5	710	2	I48668	zinc finger protei
36	103	5.5	520	2	T12487	hypothetical prote
37	102.5	5.4	2010	2	B71616	phosphatase (acid
38	101.5	5.4	829	2	B71616	DNA topoisomerase
39	101.5	5.4	1390	2	S51364	sperm tail-specific
40	101	5.4	1154	2	A39577	protein-tyrosine k
41	100	5.3	783	2	A31491	sex-determining re
42	100	5.3	2523	2	T18477	hypothetical prote
43	99.5	5.3	359	2	A46509	B cell differentia
44	99.5	5.3	4753	1	A47437	LDL-receptor-relat
45	98.5	5.2	649	2	T37740	collid-coll protei

#### ALIGNMENTS

RESULT 1  
T14029  
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum)  
N/Alternate names: erythrocyte membrane binding protein 1 (EMP1)  
C/Species: Plasmodium falciparum  
C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #ext\_change 09-Jul-2004  
C/Accession: T14029  
R/Chen, Q.; Barragan, A.; Fernandez, V.; Sundstrom, A.; Schliehterle, M.; Sahlen, A.;  
J. Exp. Med. 187, 15-23, 1998  
A/Title: Identification of Plasmodium falciparum erythrocyte membrane protein 1 (PEMP1  
A/Reference number: Z17860, MIM:9808052; PMID:9419207  
A/Accession: T14029  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-2228 <CH>  
A/Cross-references: UNIPROT:O60991; EMBL:AF003473; NID:92961467; PID:92961466; PID:MAC  
C/Genetics:  
A/Note: PCR351.2-vari

Query Match 99.6%; Score 1876; DB 2; Length 2228;  
Best Local Similarity 99.7%; Pred. No. 4.2e-124;

Matches 336; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	PCKDGGKNDVDRFSVKEQA	YDNTKMKCSNGMTCA	PPRRRLHLCNNPENNNSNDSSKAK	60
DB	79	PCKDGGKNDVDRFSVKEQA	YDNTKMKCSNGMTCA	PPRRRLHLCNNPENNNSNDSSKAK	138
QY	61	HDLLAEVCMAATYBESIKTHY	PKYDSKYPGSDPMTCTLAS	PADIGIINGRDLYLGN	120
DB	139	HDLLAEVCMAATYBESIKTHY	PKYDSKYPGSDPMTCTLAS	PADIGIINGRDLYLGN	198
QY	121	KKKQNGKETEREKLEOKLKE	IFKKIHNLKDKKAKRYNGDE	PNFYLRDMMYANRE	180
DB	199	KKKQNGKETEREKLEOKLKE	IFKKIHNLKDKKAKRYNGDE	PNFYLRDMMYANRE	258
QY	161	TWGMATSKSLDINSYFRATCN	DTGCGPSGTHNRCRCDDK	KGANAKRPKAGDGVTTIP	240
DB	259	TWGMATSKSLDINSYFRATCN	DTGCGPSGTHNRCRCDDK	KGANAKRPKAGDGVTTIP	318
QY	241	TYFDVVPQYLRWPFEMADP	CRKKKKQLENEKCRGDKS	DEYRYSRNGVDCQITSR	300
DB	319	TYFDVVPQYLRWPFEMADP	CRKKKKQLENEKCRGDKS	DEYRYSRNGVDCQITSR	378
QY	301	KGKVRMGKCTDCEPACGS	YENWIDNORQDFKQKXY	337	
DB	379	KGKVRMGKCTDCEPACGS	YENWIDNORQDFKQKXY	415	

RESULT 2  
B71600  
variant-specific surface protein 1 homolog PFB1055c - malaria parasite (Plasmodium falc  
N/Alternate names: erythrocyte membrane binding protein 1 (EMP1)

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# OM protein - protein search, using sw model

Run on: April 26, 2005, 17:50:51 ; Search time 35.9617 Seconds  
(without alignment)

3624.358 Million cell updates/sec

Title: US-09-508-967-1\_COPY\_79\_415

Sequence: 1 PCKDKGKNDVDFSVKEA.....GSYEWINDQKQPKQKKY 337

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq.1Dec04:\*

1: geneeqp1980s:\*\n2: geneeqp1990s:\*\n3: geneeqp2000s:\*\n4: geneeqp2001s:\*\n5: geneeqp2002s:\*\n6: geneeqp2003as:\*\n7: geneeqp2003bs:\*\n8: geneeqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1884	100.0	2228	2	AAW93944 P. falcip
2	894	47.5	2197	3	AAW93944 P. falcip
3	892.5	47.4	2182	2	AAW22476 P. falcip
4	892.5	47.4	2182	2	AAW22476 P. falcip
5	885	47.0	2703	2	AAW22482 P. falcip
6	885	47.0	2710	2	AAW22482 P. falcip
7	885	47.0	2710	2	AAW22482 P. falcip
8	885	47.0	3060	2	AAW22475 P. falcip
9	885	47.0	3060	2	AAW22475 P. falcip
10	868.5	46.1	1700	3	AAW77905 P. falcip
11	861	45.7	1726	2	AAW77905 P. falcip
12	861	45.7	1726	2	AAW77905 P. falcip
13	845	44.9	700	2	AAW00385 Truncated
14	845	44.9	700	2	AAW00385 Truncated
15	845	44.9	700	2	AAW22481 P. falcip
16	789	41.9	2647	8	AAW22481 P. falcip
17	653	34.7	3542	4	ADP25446 P. falcip
18	626	33.2	2459	8	ADP25446 P. falcip
19	624	33.1	302	8	ADP25446 P. falcip
20	416.5	22.1	3056	8	ADP25446 P. falcip
21	382.5	20.3	3056	8	ADP25446 P. falcip
22	379.5	19.7	362	3	AAW77912 Plasmid
23	370.5	19.1	266	8	AAW77912 Plasmid
24	360.5	19.1	411	3	AAW77913 Plasmid
25	308.5	16.4	1143	5	AAW77913 Plasmid

26	308.5	16.4	1210	6	ABG73547 P. falcip
27	284.5	15.1	572	8	ADP43693 CSA-Bind
28	281	14.9	350	5	ABD07656 P. falcip
29	281	14.9	1435	2	AAW70232 P. falcip
30	281	14.9	1435	2	AAW22477 P. falcip
31	281	14.9	1435	2	AAW22477 P. falcip
32	281	14.9	1604	2	AAW70105 P. falcip
33	281	14.9	1786	2	AAW70105 P. falcip
34	280.5	14.9	749	2	AAW70233 P. falcip
35	280.5	14.9	749	2	AAW22479 P. falcip
36	280.5	14.9	749	2	AAW22479 P. falcip
37	280.5	14.9	1086	5	AAW77901 P. falcip
38	278	14.8	557	8	ADP43694 P. falcip
39	270	14.3	616	6	ABR82499 P. falcip
40	269	14.3	616	6	ABR82499 P. falcip
41	269	14.3	1421	5	AAW76764 P. falcip
42	267	14.2	616	5	AAW50533 P. falcip
43	241	12.8	793	2	AAW70234 P. falcip
44	241	12.8	921	2	AAW22480 P. falcip
45	241	12.8	921	3	AAW77902 P. falcip

## ALIGNMENTS

RESULT 1	AAW93944 standard; protein; 2228 AA.
ID	AAW93944
XX	AAW93944;
AC	30-JUN-1999 (first entry)
DT	P. falciparum PFEEMP1 protein.
DE	P. falciparum PFEEMP1 protein.
XX	Erythrocyte membrane protein; EMP; PFEEMP1; malaria; antioocclusion;
XX	glycosaminoglycan-like moiety; antiaggregational; antimalarial;
KW	antigen receptor; infected erythrocyte; rosette formation; blood cell;
KW	capillary occlusion; cerebral malaria; treatment; vaccine; detection;
KW	medicament; parasite; diagnosis; drug screening.
XX	Plasmidium falciparum.
OS	Plasmidium falciparum.
XX	MO9915557-A1.
PN	01-APR-1999.
XX	18-SEP-1998; 98MO-SE001675.
PF	19-SEP-1997; 97SE-00003386.
XX	(KARO-) KAROLINSKA INNOVATIONS AB.
PA	Walgren M, Barragan A, Carlson J, Oljun C, Fernandez V;
PI	WPI; 1999-254692/21.
XX	New isolated malaria polypeptides.
PT	Claim 4; Page 67-74; 80pp; English.
PS	This invention describes a novel plasmidium falciparum erythrocyte
XX	membrane protein (EMP), PFEEMP1, which is capable of binding to a
CC	carbohydrate which exhibits at least one negatively charged glycosamino-
CC	glycan (GAG)-like moiety and has antiaggregational, antioocclusion and
CC	antimalarial activity. The carbohydrates of the invention are capable of
CC	acting as receptors for malaria antigens present on the surfaces of
CC	malaria infected erythrocytes, by binding to these antigens the
CC	carbohydrates prevent rosette formation by the blood cells, this prevents
CC	occlusion of capillaries as is seen in cerebral malaria caused by
CC	Plasmidium falciparum. The products of the invention can be used to treat
CC	malaria or to vaccinate against it, or used to design a model to identify
CC	compounds that bind to PFEEMP1. The carbohydrates, polypeptides and

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OM protein - protein search, using sw model

Run on: April 26, 2005, 18:03:03 ; Search time 38.7148 Seconds

(without alignments)  
3567.329 Million cell updates/sec

Title: US-09-508-967-1\_COPY\_1\_415

Perfect score: 2276

Sequence: 1 MATSGSGSGCTDDEAKHYLD.....GSYENWIDNRKPKDKKRY 415

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	956	42.0	2710	US-10-153-273-12	Sequence 12, Appl
2	845	37.1	700	US-10-153-273-10	Sequence 10, Appl
3	690	30.3	3542	US-10-087-013-2	Sequence 2, Appl
4	379.5	16.7	362	US-10-153-273-18	Sequence 18, Appl
5	360.5	15.8	411	US-10-153-273-19	Sequence 19, Appl
6	318	14.0	1143	US-09-924-154-14	Sequence 14, Appl
7	304	13.4	1435	US-10-153-273-4	Sequence 4, Appl
8	293	12.9	616	US-10-293-913A-4	Sequence 4, Appl
9	292	12.8	616	US-10-293-913A-2	Sequence 2, Appl
10	285.5	12.5	1421	US-09-924-154-13	Sequence 13, Appl
11	285.5	12.5	749	US-10-153-273-6	Sequence 6, Appl
12	285.5	12.5	1086	US-09-924-154-15	Sequence 15, Appl
13	241	10.6	921	US-10-153-273-8	Sequence 8, Appl

14	239	10.5	1115	US-10-153-273-2	Sequence 2, Appl
15	238	10.5	972	US-09-924-154-16	Sequence 16, Appl
16	233	10.2	407	US-10-087-013-8	Sequence 8, Appl
17	229.5	10.1	311	US-10-087-013-10	Sequence 10, Appl
18	218	9.6	308	US-10-087-013-11	Sequence 11, Appl
19	216.5	9.5	351	US-10-087-013-9	Sequence 9, Appl
20	216.5	9.5	1501	US-09-924-154-17	Sequence 17, Appl
21	216.5	9.5	1568	US-10-712-533A-12	Sequence 12, Appl
22	207	9.1	294	US-10-087-013-7	Sequence 7, Appl
23	197.5	8.7	411	US-10-153-273-20	Sequence 20, Appl
24	159.5	7.0	282	US-10-153-273-16	Sequence 16, Appl
25	158.5	7.0	277	US-10-153-273-15	Sequence 15, Appl
26	130.5	5.7	448	US-10-153-668-370	Sequence 370, Appl
27	126	5.5	291	US-10-153-273-13	Sequence 13, Appl
28	124	5.4	706	US-10-104-04-3843	Sequence 3843, Ap
29	121	5.3	311	US-10-153-273-21	Sequence 21, Appl
30	119.5	5.3	754	US-10-153-668-254	Sequence 254, App
31	116.5	5.1	1257	US-10-408-765A-1486	Sequence 1486, Ap
32	115.5	5.1	281	US-10-424-599-14507	Sequence 14507,
33	115.5	5.1	905	US-10-437-963-152106	Sequence 152106,
34	115	5.1	324	US-10-153-273-17	Sequence 17, Appl
35	114.5	5.0	610	US-09-989-920-212	Sequence 212, App
36	114.5	5.0	665	US-09-820-843A-107	Sequence 107, App
37	112.5	4.9	1737	US-10-437-963-194264	Sequence 194264,
38	111	4.9	1080	US-10-437-963-196386	Sequence 196386,
39	110.5	4.9	400	US-10-437-963-111221	Sequence 111221,
40	110.5	4.9	703	US-10-437-963-201481	Sequence 201481,
41	110.5	4.9	1064	US-10-220-510-1	Sequence 1, Appl
42	110	4.8	475	US-10-221-625-73	Sequence 73, Appl
43	110	4.8	933	US-10-369-493-12831	Sequence 12831, A
44	110	4.8	1903	US-10-766-993-3	Sequence 3, Appl
45	109.5	4.8	648	US-10-094-749-2472	Sequence 2472, Ap

#### ALIGNMENTS

RESULT 1  
US-10-153-273-12  
; Sequence 12, Application US/10153273  
; Publication No. US20020169305A1  
GENERAL INFORMATION:  
APPLICANT: SIm, Kim L.  
Chitnis, Chetan  
Miller, Louis H.  
Peterson, David S.  
Su, Xin-zhuang  
Wellens, Thomas E.  
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX  
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Knodbe Martens Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: California  
COUNTRY: US  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/153,273  
FILING DATE: 21-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/210,288  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Fuller, Michael  
REGISTRATION NUMBER: 36,516



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OM protein - protein search, using sw model

Run on: April 26, 2005, 17:50:53 ; Search time 11.2802 Seconds  
(without alignments)  
2746.348 Million cell updates/sec

Title: US-09-508-967-1\_COPY\_1\_415

Perfect score: 2276  
Sequence: 1 MATSGSGSGGTQDEDAKHYLD.....GSYENWIDNQRKQFDKQKKY 415

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database:

Issued Patents AA: \*  
1: /cgn2\_6/prodata/1/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/prodata/1/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/prodata/1/1aa/5A.COMB.pep: \*  
4: /cgn2\_6/prodata/1/1aa/5B.COMB.pep: \*  
5: /cgn2\_6/prodata/1/1aa/5A.COMB.pep: \*  
6: /cgn2\_6/prodata/1/1aa/5B.COMB.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1010	44.4	2182	2	US-08-487-826B-16 Sequence 16, Appl
2	956	42.0	2710	2	US-08-568-459A-12 Sequence 12, Appl
3	956	42.0	2710	2	US-08-487-826B-12 Sequence 12, Appl
4	956	42.0	2710	3	US-09-210-288-12 Sequence 12, Appl
5	956	42.0	3060	2	US-08-487-826B-14 Sequence 14, Appl
6	845	37.1	700	2	US-08-568-459A-10 Sequence 10, Appl
7	845	37.1	700	2	US-08-487-826B-10 Sequence 10, Appl
8	845	37.1	700	2	US-09-210-288-10 Sequence 10, Appl
9	379.5	16.7	362	2	US-08-568-459A-18 Sequence 18, Appl
10	379.5	16.7	362	2	US-08-487-826B-30 Sequence 30, Appl
11	379.5	16.7	362	2	US-09-210-288-18 Sequence 18, Appl
12	360.5	15.8	411	2	US-08-568-459A-19 Sequence 19, Appl
13	360.5	15.8	411	2	US-08-487-826B-31 Sequence 31, Appl
14	360.5	15.8	411	3	US-09-210-288-19 Sequence 19, Appl
15	304	13.4	1435	2	US-08-568-459A-4 Sequence 4, Appl
16	304	13.4	1435	2	US-08-487-826B-4 Sequence 4, Appl
17	304	13.4	1435	2	US-09-210-288-4 Sequence 4, Appl
18	285.5	12.5	749	2	US-08-568-459A-6 Sequence 6, Appl
19	285.5	12.5	749	2	US-08-487-826B-6 Sequence 6, Appl
20	285.5	12.5	749	3	US-09-210-288-6 Sequence 6, Appl
21	241	10.6	921	2	US-08-568-459A-8 Sequence 8, Appl
22	241	10.6	921	3	US-08-487-826B-8 Sequence 8, Appl
23	239	10.5	1115	2	US-08-568-459A-2 Sequence 2, Appl
24	239	10.5	1115	2	US-08-487-826B-2 Sequence 2, Appl
25	239	10.5	1115	3	US-09-210-288-2 Sequence 2, Appl
26	239	10.5	1115	3	US-09-210-288-2 Sequence 2, Appl
27	239	10.5	1115	6	Patent No. 5198347-6

28	239	10.5	1115	6	US-08-568-459A-20 Sequence 20, Appl
29	197.5	8.7	411	2	US-08-487-826B-32 Sequence 32, Appl
30	197.5	8.7	411	2	US-08-487-826B-32 Sequence 32, Appl
31	197.5	8.7	411	3	US-09-210-288-20 Sequence 20, Appl
32	159.5	7.0	282	2	US-08-568-459A-16 Sequence 16, Appl
33	159.5	7.0	282	2	US-08-487-826B-28 Sequence 28, Appl
34	159.5	7.0	282	3	US-09-210-288-16 Sequence 16, Appl
35	158.5	7.0	277	2	US-08-568-459A-15 Sequence 15, Appl
36	158.5	7.0	277	2	US-08-487-826B-27 Sequence 27, Appl
37	158.5	7.0	277	3	US-09-210-288-15 Sequence 15, Appl
38	150	6.6	197	6	US-08-568-459A-2 Sequence 2, Appl
39	150	6.6	197	6	US-08-487-826B-2 Sequence 2, Appl
40	150	6.6	778	6	US-09-210-288-13 Sequence 13, Appl
41	150	6.6	778	6	US-09-210-288-13 Sequence 13, Appl
42	126	5.5	291	2	US-08-568-459A-13 Sequence 13, Appl
43	126	5.5	291	3	US-08-487-826B-25 Sequence 25, Appl
44	126	5.5	291	3	US-09-210-288-13 Sequence 13, Appl
45	122.5	5.4	754	4	US-09-976-594-375 Sequence 375, App

#### ALIGNMENTS

RESULT 1  
US-08-487-826B-16  
Sequence 16, Application US/08487826B  
Patent No. 5993827  
GENERAL INFORMATION:  
APPLICANT: Sim, Kim L.  
APPLICANT: Chitnis, Chetan  
APPLICANT: Miller, Louis H.  
APPLICANT: Peterson, David S.  
APPLICANT: Su, Xin-zhan  
APPLICANT: Williams, Thomas E.  
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX  
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobb Martens Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: California  
COUNTRY: US  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487, 826B  
FILING DATE: 10-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelson, Ned  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: NIH121.001CP1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2182 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-487-826B-16  
Query Match 44.4%; Score 1010; DB 2; Length 2182;

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OM protein - protein search, using sw model

Run on: April 26, 2005, 17:50:52 ; Search time 50.4128 Seconds

(without alignments)

4215.459 Million cell updates/sec

Title: US-09-508-967-1\_COPY\_1\_415

Perfect score: 2276

Sequence: 1 MATSGSGGCTGDDAKHVD.....GSYEMTDNRKQFDKQKX 415

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter 45 summaries

Database: UniProt 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2268	99.6	2228	2	060991
2	1344	59.1	2275	2	081BX2
3	1253.5	55.1	2215	2	081BX3
4	1224	53.8	2209	2	09U0G6
5	1203.5	52.9	2215	2	081BW9
6	1139	50.0	2326	2	081IV6
7	1137.5	50.0	2152	2	081F06
8	1137.5	50.0	2201	2	081F05
9	1134	49.8	2267	2	081F05
10	1114.5	49.0	2149	2	081BK7
11	1108.5	48.7	2264	2	081BK7
12	1104	48.5	2192	2	081BW7
13	1057	46.4	2193	2	081F02
14	1049	46.1	2231	2	081F02
15	1038.5	45.6	2162	2	081EV1
16	1038.5	45.6	2207	2	081F05
17	1036	45.5	2199	2	096296
18	1031	45.3	2277	2	09U0G5
19	1031	45.3	2312	2	081IV7
20	1024	45.0	2710	2	09XZB8
21	1015	44.6	2359	2	081F19
22	1010	44.4	2182	2	026034
23	1004	44.1	2265	2	081F02
24	1003.5	44.1	2223	2	081F02
25	994.5	43.7	2646	2	081F02
26	993.5	43.7	3954	2	081F02
27	983.5	43.2	3026	2	026030
28	980	43.1	1729	2	025733
29	980	43.1	2324	2	025733
30	979	43.0	2182	2	081F04
31	978.5	43.0	2241	2	081K37

32	965.5	42.4	2135	2	061077
33	961.5	42.2	2256	2	081F05
34	957	42.0	1711	2	096108
35	956	42.0	3078	2	026031
36	952	41.8	2268	2	081F05
37	951.5	41.8	2270	2	081F05
38	947	41.6	2287	2	081F05
39	934.5	41.1	2163	2	09NFB6
40	917.5	40.3	2239	2	081BW8
41	907	39.9	2595	2	081BD8
42	899.5	39.5	2169	2	097312
43	893.5	39.3	2109	2	081F04
44	888	39.0	2181	2	081F04
45	882.5	38.8	2209	2	097324

## ALIGNMENTS

RESULT 1	060991	PRELIMINARY:	PRT: 2228 AA.
ID	060991		
AC	060991		
DT	01-AUG-1998 (TRMBLrel. 07, Created)		
DT	01-AUG-1998 (TRMBLrel. 07, Last sequence update)		
DT	01-OCT-2003 (TRMBLrel. 25, Last annotation update)		
DE	Erythrocyte membrane protein 1.		
GN	Name=FCR3S1.2-var1;		
OS	Plasmodium falciparum.		
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
OX	NCBI_TaxID=5833;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98080592; PubMed=9419207;		
RA	Chen Q., Barragan A., Fernandez V., Sundstrom A., Schlichterle M.,		
RA	Sahlen A., Carlson J., Datta S., Wahlgren M.,		
RT	"Identification of Plasmodium falciparum erythrocyte membrane protein 1 (PFEMP1) as the rosetting ligand of the malaria parasite P.		
RT	falciparum."		
RT	J. Exp. Med. 187:15-23(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Chen Q.J., Wahlgren M.,		
RL	Submitted (May-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF003473; AAC05730.1; -		
DR	PIR; T14029; T14029		
DR	GO; GO:0005539; F:glycosaminoglycan binding; IEA.		
DR	GO; GO:0009405; P:patogenesis; IEA.		
DR	InterPro; IPR004258; PFEMP.		
DR	Pfam; PF03011; PFEMP; 2.		
SQ	SEQUENCE 2228 AA; 252811 MW; 5D8C8B9FA22DC8B CRC64;		
Query Match	99.6%; Score 2268; DB 2; Length 2228;		
Best local Similarity	99.8%; Pred. No. 6,7e-144;		
Matches	414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Qy	1	MATSGSGCTGDDAKHVDLAEVCAAAKYEBSITTHYPKDYSGDFPACTLAR	60
Db	1	MATSGSGCTGDDAKHVDLAEVCAAAKYEBSITTHYPKDYSGDFPACTLAR	60
Qy	61	MOTESKYTELEANSKRNPKCKGKNDVDRFSYKQAGYDNKMKKSGNGTCAFPRLH	120
Db	61	MOTESKYTELEANSKRNPKCKGKNDVDRFSYKQAGYDNKMKKSGNGTCAFPRLH	120
Qy	121	LCNNFPNNNSNSSRKXKDLAEVCAAAKYEBSITTHYPKDYSGDFPACTLAR	180
Db	121	LCNNFPNNNSNSSRKXKDLAEVCAAAKYEBSITTHYPKDYSGDFPACTLAR	180
Qy	181	SPADIGIIRGRDLYLGNKKKNGKTEREKLEQKLEIFKKIHNLKQBEAKRYNGD	240
Db	181	SPADIGIIRGRDLYLGNKKKNGKTEREKLEQKLEIFKKIHNLKQBEAKRYNGD	240
Qy	241	EDRFYKLRDWMWTANRETWGAMTCSKEIDNSYFPATCNTDGTGQSPQTHNRCRCDKK	300

Db 361 EYRYCSRNGYDCEOTISRKGVRMGCGCTDCFFACHSYENWIDNORKOEDKOKY 415

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OM protein - protein search, using sw model

Run on: April 26, 2005, 17:50:51 ; Search time 44.2852 Seconds

(without alignments)  
3624.358 Million cell updates/sec

Title: US-09-508-967-1\_COPY\_1\_415

Perfect score: 2276  
Sequence: 1 MATSGSGGGTQDEDAKHVD.....GSYENWIDQKQKFKQKRY 415

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_16Dec04:\*

1: geneseqp19808:\*\n2: geneseqp19908:\*\n3: geneseqp20008:\*\n4: geneseqp20018:\*\n5: geneseqp20028:\*\n6: geneseqp20038:\*\n7: geneseqp20038:\*\n8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2376	100.0	2228	AAW93944	AAW93944 P. falcip
2	1036	45.5	2197	AAI18352	AAI18352 Plasmodiu
3	1010	44.4	2182	AAW22476	AAW22476 Plasmodiu
4	1010	44.4	2182	AAW77906	AAW77906 Plasmodiu
5	972	42.7	1726	AAW00385	AAW00385 Truncated
6	972	42.7	1726	AAW00385	AAW00385 Truncated
7	957	42.0	1700	AAI18144	AAI18144 Plasmodiu
8	956	42.0	2703	AAW70236	AAW70236 P. falcip
9	956	42.0	2710	AAW22482	AAW22482 Plasmodiu
10	956	42.0	2710	AAW77904	AAW77904 P. falcip
11	956	42.0	3060	AAW22475	AAW22475 Plasmodiu
12	956	42.0	3060	AAW77905	AAW77905 Plasmodiu
13	871.5	38.3	2647	ADP25446	ADP25446 Plasmodiu
14	845	37.1	700	AAW70235	AAW70235 P. falcip
15	845	37.1	700	AAW22481	AAW22481 Plasmodiu
16	845	37.1	700	AAW77903	AAW77903 P. falcip
17	690	30.3	3542	AAW62142	AAW62142 P. falcip
18	676	29.7	2459	ADP69969	ADP69969 Plasmodiu
19	624	27.4	302	ADP69970	ADP69970 Plasmodiu
20	421	18.5	3056	ADR43499	ADR43499 CSA-bind
21	382.5	16.8	301	ADP69973	ADP69973 Plasmodiu
22	379.5	16.7	362	AAW77912	AAW77912 Plasmodiu
23	370.5	16.3	266	ADP69971	ADP69971 Plasmodiu
24	360.5	15.8	411	AAW77913	AAW77913 Plasmodiu
25	318	14.0	1143	AAU76759	AAU76759 Plasmodiu

26	318	14.0	1210	6	ABG73547	ABG73547 P. falcip
27	304	13.4	1435	2	AAW70232	AAW70232 P. falcip
28	304	13.4	1435	2	AAW22477	AAW22477 Silastic ac
29	304	13.4	1435	3	AAW77900	AAW77900 P. falcip
30	304	13.4	1604	2	AAW70105	AAW70105 TNF-R-EB
31	304	13.4	1786	2	AAW41043	AAW41043 CD4-EB
32	293	12.9	616	6	ABR82499	ABR82499 Synthetic
33	292	12.8	1421	6	ABR82498	ABR82498 Synthetic
34	292	12.8	1421	5	AAU76764	AAU76764 Plasmodiu
35	290	12.7	616	5	AAW50533	AAW50533 Unidentif
36	286.5	12.6	572	8	ADR43593	ADR43593 CSA-bind
37	285.5	12.5	749	2	AAW70233	AAW70233 P. falcip
38	285.5	12.5	749	2	AAW22479	AAW22479 Plasmodiu
39	285.5	12.5	749	3	AAW77901	AAW77901 P. falcip
40	285.5	12.5	1086	5	AAU76760	AAU76760 Plasmodiu
41	281	12.3	350	5	ABW07656	ABW07656 P. falcip
42	280	12.3	557	8	ADR43594	ADR43594 CSA-bind
43	249.5	11.0	1245	2	AAW70106	AAW70106 TNF-R-Pl
44	241	10.6	793	2	AAW70234	AAW70234 P. falcip
45	241	10.6	921	2	AAW22480	AAW22480 Plasmodiu

## ALIGNMENTS

RESULT 1  
AAW93944  
ID AAW93944 standard; protein; 2228 AA.

AAW93944;

30-JUN-1999 (first entry)

P. falciparum PfEMP1 protein.

Erythrocyte membrane protein; EMP; PfEMP1; malaria; antioclusional;  
glycosaminoglycan-like moiety; antiaggregational; antimalarial;  
antigen receptor; infected erythrocyte; rosette formation; blood cell;  
capillary occlusion; cerebral malaria; treatment; vaccine; detection;  
medicament; parasite; diagnosis; drug screening.

Plasmodium falciparum.

WO9915557-A1.

01-APR-1999.

18-SEP-1998; 98WO-SE001675.

19-SEP-1997; 97SE-00003386.

(KARO-) KAROLINSKA INNOVATIONS AB.

Wahlgren M, Barragan A, Carlson J, Qijun C, Fernandez V;

WPI; 1999-254692/21.

New isolated malaria polypeptides.

Claim 4; Page 67-74; 80pp; English.

This invention describes a novel Plasmodium falciparum erythrocyte membrane protein (EMP), PfEMP1, which is capable of binding to a carbohydrate which exhibits at least one negatively charged glycosaminoglycan (GAG)-like moiety and has antiaggregational, antioclusional and antimalarial activity. The carbohydrates of the invention are capable of acting as receptors for malaria antigens present on the surfaces of malaria infected erythrocytes, by binding to these antigens the carbohydrates prevent rosette formation by the blood cells, this prevents occlusion of capillaries as is seen in cerebral malaria caused by Plasmodium falciparum. The products of the invention can be used to treat malaria or to vaccinate against it, or used to design a model to identify compounds that bind to PfEMP1. The carbohydrates, polypeptides and

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OM protein - protein search, using sw model

Run on: April 26, 2005, 18:03:03 ; Search time 207.847 Seconds

(without alignments)  
3567.329 Million cell updates/sec

Title: US-09-508-967-1

Perfect score: 12100  
Sequence: 1 MATSGSGGCTQDDAKHVL.....VNNKEIFEEYPSIDWNI 2228

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
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4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
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19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3197.5	26.4	2710	US-10-153-273-12	Sequence 12, Appl
2	1681.5	13.9	3542	US-10-087-013-2	Sequence 2, Appl
3	1385	11.4	700	US-10-153-273-10	Sequence 10, Appl
4	702	5.8	921	US-10-153-273-8	Sequence 8, Appl
5	445	3.7	311	US-10-087-013-10	Sequence 10, Appl
6	439.5	3.6	407	US-10-087-013-8	Sequence 8, Appl
7	422	3.5	294	US-10-087-013-7	Sequence 7, Appl
8	421.5	3.5	1421	US-09-924-154-13	Sequence 13, Appl
9	418	3.5	1435	US-10-153-273-4	Sequence 4, Appl
10	396	3.3	1086	US-09-924-154-15	Sequence 15, Appl
11	386	3.2	308	US-10-087-013-11	Sequence 11, Appl
12	379.5	3.1	362	US-10-153-273-18	Sequence 18, Appl
13	376	3.1	1501	US-09-924-154-17	Sequence 17, Appl

14	376	3.1	1568	US-10-712-533A-12	Sequence 12, Appl
15	375	3.1	351	US-10-087-013-9	Sequence 9, Appl
16	371.5	3.1	1143	US-09-924-154-14	Sequence 14, Appl
17	360.5	3.0	411	US-10-153-273-19	Sequence 19, Appl
18	345.5	2.9	749	US-10-153-273-6	Sequence 6, Appl
19	324.5	2.7	616	US-10-293-913A-4	Sequence 4, Appl
20	323.5	2.7	616	US-10-293-913A-2	Sequence 2, Appl
21	315	2.6	1115	US-10-153-273-2	Sequence 2, Appl
22	295.5	2.4	5176	US-10-437-963-150986	Sequence 150986,
23	284	2.3	6642	US-10-369-493-5013	Sequence 5013, Ap
24	282.5	2.3	3507	US-10-369-493-5784	Sequence 5784, Ap
25	273	2.3	10203	US-10-661-809-23	Sequence 23, Appl
26	271	2.2	6641	US-10-282-122A-70580	Sequence 70580, A
27	266.5	2.2	2492	US-10-697-526-2	Sequence 2, Appl
28	265.5	2.2	1639	US-10-087-464-10	Sequence 10, Appl
29	263	2.2	3692	US-10-282-122A-71235	Sequence 71235, A
30	259.5	2.1	2052	US-10-282-122A-51602	Sequence 51602, A
31	259	2.1	972	US-09-924-154-16	Sequence 16, Appl
32	258	2.1	3225	US-10-408-765A-254	Sequence 254, App
33	257.5	2.1	5560	US-10-263-929-142	Sequence 142, App
34	254.5	2.1	2785	US-09-801-574-8	Sequence 8, Appl
35	251.5	2.1	1743	US-09-882-227-624	Sequence 624, App
36	251.5	2.1	2476	US-09-824-574-7	Sequence 7, Appl
37	251.5	2.1	3051	US-10-144-194A-62	Sequence 62, Appl
38	249	2.1	2062	US-10-052-648A-52	Sequence 52, Appl
39	248	2.0	1903	US-10-766-993-3	Sequence 3, Appl
40	245.5	2.0	1038	US-10-282-122A-43827	Sequence 43827, A
41	245.5	2.0	2781	US-10-263-929-122	Sequence 122, App
42	245	2.0	2375	US-10-408-765A-277	Sequence 277, App
43	243.5	2.0	2058	US-10-052-648A-20	Sequence 20, Appl
44	242.5	2.0	2481	US-10-282-122A-43762	Sequence 43762, A
45	239.5	2.0	4688	US-10-282-122A-76865	Sequence 76865, A

## ALIGNMENTS

RESULT 1  
US-10-153-273-12  
; Sequence 12, Application US/10153273  
; Publication No. US20020169305A1  
GENERAL INFORMATION:  
APPLICANT: Sim, Kim L.  
Chilnis, Chetan  
Miller, Louis H.  
Peterson, David S.  
Su, Xin-zhuan  
Wellms, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX  
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe Martens Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: California  
COUNTRY: US  
ZIP: 92660

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/153, 273  
FILING DATE: 21-May-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/210, 288  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Fuller, Michael  
REGISTRATION NUMBER: 36,516

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: April 26, 2005, 17:50:53 ; Search time 60.5597 Seconds  
(without alignment)  
2746.348 Million cell updates/sec

Title: US-09-508-967-1  
Perfect score: 12100  
Sequence: 1 NATSGSGSGTQDEDAKHVID.....VNKKEIFEERYPSIDINNI 2228

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/prodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4817	39.8	2182	2	US-08-487-826B-16
2	4802	39.7	3060	2	US-08-487-826B-14
3	3197.5	26.4	2710	2	US-08-568-459A-12
4	3197.5	26.4	2710	2	US-08-487-826B-12
5	3197.5	26.4	2710	2	US-09-210-288-12
6	1385	11.4	700	2	US-08-568-459A-10
7	1385	11.4	700	2	US-08-487-826B-10
8	1385	11.4	700	2	US-09-210-288-10
9	702	5.8	921	2	US-08-568-459A-8
10	702	5.8	921	2	US-08-487-826B-8
11	702	5.8	921	2	US-09-210-288-8
12	418	3.5	1435	2	US-08-568-459A-4
13	418	3.5	1435	2	US-08-487-826B-4
14	418	3.5	1435	2	US-09-210-288-4
15	379.5	3.1	362	2	US-08-568-459A-18
16	379.5	3.1	362	2	US-08-487-826B-30
17	379.5	3.1	362	2	US-09-210-288-18
18	360.5	3.0	411	2	US-08-568-459A-19
19	360.5	3.0	411	2	US-08-487-826B-31
20	360.5	3.0	411	2	US-09-210-288-19
21	345.5	2.9	749	2	US-08-568-459A-6
22	345.5	2.9	749	2	US-08-487-826B-6
23	345.5	2.9	749	2	US-09-210-288-6
24	315	2.6	1115	2	US-08-568-459A-2
25	315	2.6	1115	2	US-08-487-826B-2
26	315	2.6	1115	2	US-09-210-288-2
27	315	2.6	1115	6	5198347-6

28	315	2.6	1115	6	5198347-6
29	311.5	2.6	1663	5	PCT-US93-07261-16
30	288	2.4	1588	5	PCT-US93-07261-11
31	272.5	2.3	2907	4	US-09-698-295-1
32	272	2.2	10182	3	US-09-134-001C-3159
33	267	2.2	5024	4	US-09-710-279-2864
34	265	2.2	3696	3	US-09-134-001C-5080
35	262.5	2.2	3969	3	US-08-061-376-5
36	262.5	2.2	3969	4	US-09-538-092-1262
37	258	2.1	3259	4	US-09-949-016-6507
38	251.5	2.1	2476	4	US-09-824-574-7
39	249.5	2.1	2349	4	US-09-538-092-914
40	245.5	2.0	2781	4	US-09-698-295-10
41	245	2.0	2375	4	US-09-538-092-1131
42	244.5	2.0	2004	4	US-09-538-092-1371
43	244.5	2.0	2004	4	US-09-949-016-6756
44	243.5	2.0	2733	4	US-09-949-016-11433
45	241.5	2.0	2186	4	US-09-949-016-10828

## ALIGNMENTS

RESULT 1  
US-08-487-826B-16  
Sequence 16, Application US/08487826B  
Patent No. 5993827  
GENERAL INFORMATION:  
APPLICANT: Sim, Kim L.  
APPLICANT: Chitnis, Chetan  
APPLICANT: Miller, Louis H.  
APPLICANT: Peterson, David S.  
APPLICANT: Su, Xin-zhaun  
APPLICANT: Wellems, Thomas E.  
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX  
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Knobbe Martens Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: California  
COUNTRY: US  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,826B  
FILING DATE: 10-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelsen, Ned  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: NIH121.001CP1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2182 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-487-826B-16  
Query Match 39.8%; Score 4817; DB 2; Length 2182;

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# OM protein - protein search, using SW model

Run on: April 26, 2005, 17:50:52 ; Search time 270.65 Seconds  
(without alignment)

4215.459 Million cell updates/sec

Title: US-09-508-967-1

Perfect score: 12100

Sequence: 1 MATSGSGSGGTQDEDAKHVD.....VANKKIFEEYPISDINNI 2228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12065	99.7	2228	2	060991 plasmodium
2	5680.5	46.9	2231	2	081A84 plasmodium
3	5407.5	44.7	2215	2	081BX3 plasmodium
4	5285.5	43.7	2215	2	081BW9 plasmodium
5	5220	43.1	2192	2	081BW7 plasmodium
6	5216.5	43.1	2277	2	09U0G5 plasmodium
7	5159	42.6	2275	2	081BX2 plasmodium
8	5073	41.9	2199	2	096296 plasmodium
9	4979	41.1	2259	2	081519 plasmodium
10	4962.5	41.0	2287	2	081520 plasmodium
11	4915	40.6	2207	2	081495 plasmodium
12	4901	40.5	3078	2	026031 plasmodium
13	4817	39.8	2182	2	026034 plasmodium
14	4809.5	39.7	2210	2	09X2B8 plasmodium
15	4786.5	39.6	2223	2	081D12 plasmodium
16	4741.5	39.2	2241	2	081K37 plasmodium
17	4728	39.1	2193	2	081FQ2 plasmodium
18	4721.5	39.0	2267	2	081BX1 plasmodium
19	4711	38.9	2664	2	026033 plasmodium
20	4706	38.9	2256	2	0815L5 plasmodium
21	4690	38.8	2182	2	081E1V plasmodium
22	4659.5	38.5	2162	2	081E1V plasmodium
23	4648.5	38.4	2209	2	09U0G6 plasmodium
24	4648	38.4	2264	2	0812E3 plasmodium
25	4606	38.1	2326	2	081I16 plasmodium
26	4602	38.0	2238	2	081E20 plasmodium
27	4583	38.0	2646	2	081220 plasmodium
28	4583	37.9	2595	2	081521 plasmodium
29	4565	37.7	2646	2	081BD8 plasmodium
30	4538.5	37.5	2265	2	081A83 plasmodium
31	4498.5	37.2	2149	2	081FK7 plasmodium

32	4493.5	37.1	2163	2	09NFB6 plasmodium
33	4464.5	36.9	2109	2	081A87 plasmodium
34	4432	36.6	2212	2	081I17 plasmodium
35	4418.5	36.5	2201	2	081F05 plasmodium
36	4381	36.2	2152	2	081F06 plasmodium
37	4346.5	35.9	2203	2	0812C4 plasmodium
38	4341.5	35.9	2169	2	097312 plasmodium
39	4310.5	35.6	2178	2	081643 plasmodium
40	4302.5	35.6	2209	2	097324 plasmodium
41	4285	35.4	2268	2	0814N5 plasmodium
42	4270.5	35.3	2270	2	0813E5 plasmodium
43	4268.5	35.3	2215	2	081I26 plasmodium
44	4267.5	35.3	2239	2	081BW8 plasmodium
45	4210	34.8	2120	2	081AK1 plasmodium

## ALIGNMENTS

RESULT 1	060991	PRELIMINARY;	PRT; 2228 AA.
ID	060991		
AC	060991		
DT	01-AUG-1998 (TREMBLrel. 07, Created)		
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Erythrocyte membrane protein 1.		
GN	Name=PCR351.2-var1;		
OS	Plasmodium falciparum.		
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
OX	NCBI_TaxID=5833;		
RM	(1)		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98080592; PubMed=9419207;		
RA	Chen Q., Barragan A., Fernandez V., Sundstrom A., Schlichterle M.,		
RA	Sahlen A., Carlson J., Datta S., Wahlgren M.,		
RT	Identification of Plasmodium falciparum erythrocyte membrane protein 1 (PFEMP1) as the resetting ligand of the malaria parasite P.		
RT	falciparum."		
RT	J. Exp. Med. 187:15-23(1998).		
RL	(2)		
RP	SEQUENCE FROM N.A.		
RA	Chen Q.J., Wahlgren M.,		
RL	Submitted (May-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF003473; AAC05730.1; -		
DR	PIR; T14029; T14029.		
DR	GO; GO:0005539; P:glycosaminoglycan binding; IEA.		
DR	GO; GO:0009405; P:patogenesis; IEA.		
DR	InterPro; IPR004258; PFEMP.		
DR	Pfam; PF03011; PFEMP; 2.		
SO	SEQUENCE 2228 AA; 252811 MW; 5D8C8E9BFA22DC8B CRC64;		
Query Match	99.7%; Score 12065; DB 2; Length 2228;		
Best local similarity	99.8%; Pred. No. 0;		
Matches 2223; Conservative	0; Mismatches	5; Indels	0; Gaps
Oy	1	MATSGSGSGGTQDEDAKHVDLFEFGQKVDVHGEAKNVYSELKSLASLIGETAFYKS	60
Db	1	MATSGSGSGGTQDEDAKHVDLFEFGQKVDVHGEAKNVYSELKSLASLIGETAFYKS	60
Oy	61	MOTSSKTELLEANSKKNPKCKGKNDVDRFSVKEQAGYDNKKKCSNGMTCAFPRLH	120
Db	61	MOTSSKTELLEANSKKNPKCKGKNDVDRFSVKEQAGYDNKKKCSNGMTCAFPRLH	120
Oy	121	LCNNKFPNNNSNNSKXKHDLAEVCAAYEGESITHTYPKYDSTKPGSDPFCITLAR	180
Db	121	LCNNKFPNNNSNNSKXKHDLAEVCAAYEGESITHTYPKYDSTKPGSDPFCITLAR	180
Oy	181	SPADIGIIRGRDYLGNKKKKQNGKTEREKLQKLKBIFKCIHDNLADKBAQKRYNGD	240
Db	181	SPADIGIIRGRDYLGNKKKKQNGKTEREKLQKLKBIFKCIHDNLADKBAQKRYNGD	240
Oy	241	EDRPFYLRDWDWTARRETWGMATCKSKELDNSSYPATCNDGQGGSPQTHKCRCDKX	300

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# OM protein - protein search, using sw model

Run on: April 26, 2005, 17:50:53 ; Search time 43.3638 Seconds

(without alignments)  
4943.551 Million cell updates/sec

Title: US-09-508-967-1

Perfect score: 12100

Sequence: 1 MATSGSGGCTODEDAKHVLD.....VNKKKIFEEBYPISDIWNT 2228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first: 45 summaries

## Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	12065	99.7	2228	2	T14029	variant-specific s
2	5074	41.9	2197	2	E71600	variant-specific s
3	4901	40.5	3078	2	T28432	variant-specific s
4	4817	39.8	2182	2	T28634	variant-specific s
5	4711	38.9	2664	2	T28626	variant-specific s
6	4084	33.8	2647	2	T28161	hypothetical prote
7	4073	33.7	2042	2	T18399	variant-specific s
8	3989	33.0	3006	2	T28625	variant-specific s
9	3937	32.5	2924	2	T18378	variant-specific s
10	3297.5	27.3	1711	2	C71625	variant-specific s
11	3192	26.4	2706	2	T28155	variant-specific s
12	2959	24.5	1278	2	T18396	erythrocyte membra
13	2863	23.7	2212	2	T28157	erythrocyte membra
14	2668	22.0	3026	2	T28431	variant surface pr
15	2518	20.8	2135	2	T14602	variant-specific s
16	1319.5	10.9	431	2	F71600	variant-specific s
17	782	6.5	440	2	E71625	variant-specific s
18	418	3.5	1435	2	A37793	erythrocyte-bindin
19	406	3.4	248	2	C71624	variant-specific s
20	360	3.0	4550	2	T18440	hypothetical prote
21	339	2.8	1526	2	A45601	mature-parasite-in
22	329.5	2.7	3394	2	T18501	hypothetical prote
23	321.5	2.7	2523	2	T18472	hypothetical prote
24	321	2.7	2441	2	D71623	erythrocyte membra
25	318.5	2.6	2401	2	T28676	hypothetical prote
26	315	2.6	1070	2	T30848	Duffy receptor - p
27	310.5	2.6	1979	2	C71622	hypothetical prote
28	303	2.5	2269	2	T28677	rhodopsin protein -
29	301	2.5	2829	2	A42771	reticulocyte-bindi

30	300.5	2.5	3724	2	T18427	hypothetical prote
31	287	2.4	1308	2	E71622	probable membrane
32	285	2.4	1871	2	D96796	probable heat shoc
33	284	2.3	6642	2	T29757	protein UNC-89 - C
34	283.5	2.3	3844	2	T18402	asparagine/aspara
35	282.5	2.3	3507	2	T34513	hypothetical prote
36	279.5	2.3	1939	2	T18372	repeat organellar
37	277.5	2.3	1658	2	S55101	hypothetical prote
38	271	2.2	2485	1	H71621	hypothetical prote
39	269.5	2.2	1631	1	SAZOK1	serine/chreonine-s
40	267.5	2.2	1726	2	A45948	major merozoite su
41	265.5	2.2	1639	2	S05603	major merozoite su
42	265	2.2	2657	2	T18497	major merozoite su
43	263.5	2.2	1640	2	A24594	hypothetical prote
44	262.5	2.2	1045	2	T18373	probable major sur
45	262.5	2.2	1726	1	SAZOKM	erythrocyte bindin
						major merozoite su

## ALIGNMENTS

### RESULT 1

T14029

variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum)

N/Alternate names: erythrocyte membrane binding protein 1 (EMP1)

C/Species: Plasmodium falciparum

C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C/Accession: T14029

R/Chen, O.; Barragan, A.; Fernandez, V.; Sundstrom, A.; Schlichterle, M.; Sahlen, A.; C

J. Exp. Med. 187, 15-23, 1998

A/Title: Identification of Plasmodium falciparum erythrocyte membrane protein 1 (PEMP1)

A/Reference number: Z17860; WUID:98080592; PMID:9419207

A/Accession: T14029

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: mRNA

A/Residues: 1-2228 <CHS>

A/Cross-references: UNIPROT:O60991; EMBL:AF003473; NID:92961467; PID:92961468; PIDN:AC0

C/Genetic:

A/Note: PCR351.2-var1

Query Match	99.7%	Score 12065	DB 2	Length 2228
Best Local Similarity	99.8%	Pred. No. 0		
Matches 2223	Conservative 0	Mismatches 5	Indels 0	Gaps 0
QY	1	MATSGSGGCTODEDAKHVLD	FEFGQKVHDEHGEAKNYVELKGSLSIASILGETAFYKS	60
DB	1	MATSGSGGCTODEDAKHVLD	FEFGQKVHDEHGEAKNYVELKGSLSIASILGETAFYKS	60
QY	61	MOTESKYTELIANSKRNPCCKD	KGNDVDRPSVYEQAGYDNKKKCSNGMTCAFPRLH	120
DB	61	MOTESKYTELIANSKRNPCCKD	KGNDVDRPSVYEQAGYDNKKKCSNGMTCAFPRLH	120
QY	121	LNNKPNPNNSNDSSKAGHD	LAIVCAAKYGEISIKTHYPYDYSKYPSGDPKMTLAR	180
DB	121	LNNKPNPNNSNDSSKAGHD	LAIVCAAKYGEISIKTHYPYDYSKYPSGDPKMTLAR	180
QY	181	SPADIGDIIIRGDLVYGNK	KKKQNGKETERBEKLEKQIKIPKGIHNDLMDKRAORRYND	240
DB	181	SPADIGDIIIRGDLVYGNK	KKKQNGKETERBEKLEKQIKIPKGIHNDLMDKRAORRYND	240
QY	241	EDPNFYKLRBDWWTANRE	TWGCAMTCSKELDNSSYFRATCNDTGGQPSQTHNKRCDKX	300
DB	241	EDPNFYKLRBDWWTANRE	TWGCAMTCSKELDNSSYFRATCNDTGGQPSQTHNKRCDKX	300
QY	301	GANNKPRAGGDDVITV	TFDYVPOYLWPEBMAEDCRKKKGLLEWLEKQCKDKSD	360
DB	301	GANNKPRAGGDDVITV	TFDYVPOYLWPEBMAEDCRKKKGLLEWLEKQCKDKSD	360
QY	361	EYRYSRNGYDCEQITIS	RKGRVWGKGTDCFPACGSENNIDNORQKQKTYKIS	420
DB	361	EYRYSRNGYDCEQITIS	RKGRVWGKGTDCFPACGSENNIDNORQKQKTYKIS	420
QY	421	DGGGRKRAVGQITTY	EGEYKSFYEKLNDGYSYVDAFLGLNNEKAKCKDITDGGKINF	480
DB	421	DGGGRKRAVGQITTY	EGEYKSFYEKLNDGYSYVDAFLGLNNEKAKCKDITDGGKINF	480



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# OM protein - protein search, using sw model

Run on: April 26, 2005, 17:50:51 ; Search time 237.753 Seconds  
(without alignments)  
3624.358 Million cell updates/sec

Title: US-09-508-967-1

Perfect score: 12100  
Sequence: 1 MNTSGSGSGTQEDAHVLD.....VNKKKIFEEYPSIDWNI 2228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_15Dec04:.\*  
1: geneSeq19808:.\*  
2: geneSeq19908:.\*  
3: geneSeq20008:.\*  
4: geneSeq20018:.\*  
5: geneSeq20028:.\*  
6: geneSeq20038:.\*  
7: geneSeq20038:.\*  
8: geneSeq20048:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12100	100.0	2228	2	AAW93944 P. falcip
2	5074	41.9	2197	3	AAW18352 Plasmodi
3	4817	39.8	2182	3	AAW22476 Plasmodi
4	4817	39.8	2182	3	AAW77906 Plasmodi
5	4802	39.7	3060	2	AAW22475 Plasmodi
6	4802	39.7	3060	2	AAW77905 Plasmodi
7	4084	33.8	2647	8	ADP25446 Plasmodi
8	3928.5	32.5	2913	2	AAW00384 Plasmodi
9	3197.5	26.4	2710	2	AAW70236 P. falcip
10	3197.5	26.4	2710	3	AAW22482 Plasmodi
11	3197.5	26.4	2710	3	AAW77904 P. falcip
12	2929.5	24.2	1726	3	AAW00385 Plasmodi
13	2497	20.6	1700	3	AAW18144 P. falcip
14	1681.5	13.9	3542	4	AAW22482 Plasmodi
15	1555	12.9	2459	8	ADP25446 Plasmodi
16	1529.5	12.6	3056	8	ADP25446 Plasmodi
17	1385	11.4	700	2	AAW70235 P. falcip
18	1385	11.4	700	2	AAW22481 Plasmodi
19	1385	11.4	700	3	AAW77903 P. falcip
20	1319.5	10.9	431	3	AAW18350 Plasmodi
21	782	6.5	440	3	AAW18146 Plasmodi
22	702	5.8	921	3	AAW22480 Plasmodi
23	702	5.8	921	3	AAW77902 P. falcip
24	697	5.8	793	2	AAW70234 P. falcip
25	624	5.2	302	8	ADP25446 Plasmodi

26	591	4.9	445	4	AAW66344 Malari
27	449	3.7	437	8	ADP25446 Plasmodi
28	445	3.7	311	4	AAW62150 P. falcip
29	439.5	3.6	407	4	AAW62148 P. falcip
30	428.5	3.5	1604	2	AAW70105 TNP-R-EBA
31	425	3.5	1786	2	AAW41043 CD4-RBA17
32	422	3.5	294	4	AAW62147 P. falcip
33	421.5	3.5	1421	5	AAW70232 P. falcip
34	418	3.5	1435	2	AAW22477 P. falcip
35	418	3.5	1435	2	AAW22477 P. falcip
36	418	3.5	1435	2	AAW77900 P. falcip
37	406	3.4	248	3	AAW18151 Plasmodi
38	396	3.3	1086	5	AAW76760 Plasmodi
39	386	3.2	308	4	AAW62151 P. falcip
40	382.5	3.2	301	8	ADP25446 Plasmodi
41	379.5	3.1	362	3	AAW77912 Plasmodi
42	377.5	3.1	245	8	ADP25446 Plasmodi
43	376	3.1	1501	5	AAW76762 Plasmodi
44	376	3.1	1568	6	AAW70152 Amino aci
45	375	3.1	351	4	AAW62149 P. falcip

## ALIGNMENTS

RESULT 1  
ID AAW93944 standard; protein; 2228 AA.  
AC AAW93944;  
DT 30-JUN-1999 (first entry)  
DB P. falciparum PfEMP1 protein.  
KW Erythrocyte membrane protein; EMP; PfEMP1; malaria; antileishmanial;  
KW glycosaminoglycan-like moiety; antileishmanial; antimalarial;  
KW antigen receptor; infected erythrocyte; rosette formation; blood cell;  
KW capillary occlusion; cerebral malaria; treatment; vaccine; detection;  
KW medicament; parasite; diagnosis; drug screening.  
OS Plasmodium falciparum.  
XX WO9915557-A1.  
XX PN 01-APR-1999.  
XX PD 18-SEP-1998; 98WO-SE001675.  
XX PP 19-SEP-1997; 97SE-00003386.  
XX PR (KARO-) KAROLINSKA INNOVATIONS AB.  
XX PI Wahlgren M, Barragan A, Carlson J, Qijun C, Fernandez V,  
XX WPI; 1999-254692/21.  
XX DR New isolated malaria polypeptides.  
XX PT Claim 4; Page 67-74; 80pp; English.  
XX PS This invention describes a novel Plasmodium falciparum erythrocyte  
XX membrane protein (EMP), PfEMP1, which is capable of binding to a  
XX carbohydrate which exhibits at least one negatively charged glycosamino-  
XX glycan (GAG)-like moiety and has antileishmanial, antileishmanial and  
XX acting as receptors for malaria antigens present on the surfaces of  
XX malaria infected erythrocytes, by binding to these antigens the  
XX carbohydrates prevent rosette formation by the blood cells, this prevents  
XX occlusion of capillaries as is seen in cerebral malaria caused by  
XX Plasmodium falciparum. The products of the invention can be used to treat  
XX malaria or to vaccinate against it, or used to design a model to identify  
XX compounds that bind to PfEMP1. The carbohydrates, polypeptides and